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SEQUENCE LISTING

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<120> NOVEL SERINE PROTEASE BSSP5

<130> UEMURA=5

<140> 09/856,319
<141> 2001-05-21

<150> JP 10/347806
<151> 1998-11-20

<150> PCT JP99/06473
<151> 1999-11-19

<160> 32

<170> PatentIn version 3.1

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ggc tcc tcc tgg ggc tgc ggc att cct gcc atc aaa ccg gca ctg agc 97
Gly Ser Ser Trp Gly Cys Gly Ile Pro Ala Ile Lys Pro Ala Leu Ser
-20 -15 -10 -5

ttc agc cag agg att gtc aac ggg gag aat gca gtg ttg ggc tcc tgg 145
Phe Ser Gln Arg Ile Val Asn Gly Glu Asn Ala Val Leu Gly Ser Trp
-1 1 5 10

ccc tgg cag gtg tcc ctg cag gac agc agc ggc ttc cac ttc tgc ggt 193
Pro Trp Gln Val Ser Leu Gln Asp Ser Ser Gly Phe His Phe Cys Gly
15 20 25

ggt tct ctc atc agc cag tcc tgg gtg gtc act gct gcc cac tgc aat 241 ✓
Gly Ser Leu Ile Ser Gln Ser Trp Val Val Thr Ala Ala His Cys Asn
30 35 40

gtc agc cct ggc cgc cat ttt gtt gtc ctg ggc gag tat gac cga tca 289
Val Ser Pro Gly Arg His Phe Val Val Leu Gly Glu Tyr Asp Arg Ser

45	50	55	60	
tca aac gca gag ccc ttg cag gtt ctg tcc gtc tct cgg gcc att aca				337
Ser Asn Ala Glu Pro Leu Gln Val Leu Ser Val Ser Arg Ala Ile Thr	65	70	75	
cac cct agc tgg aac tct acc acc atg aac aat gac gtg acg ctg ctg				385
His Pro Ser Trp Asn Ser Thr Thr Met Asn Asn Asp Val Thr Leu Leu	80	85	90	
aag ctc gcc tcg cca gcc cag tac aca aca cgc atc tcg cca gtt tgc				433
Lys Leu Ala Ser Pro Ala Gln Tyr Thr Thr Arg Ile Ser Pro Val Cys	95	100	105	
ctg gca tcc tca aac gag gct ctg act gaa ggc ctc acg tgt gtc acc				481
Leu Ala Ser Ser Asn Glu Ala Leu Thr Glu Gly Leu Thr Cys Val Thr	110	115	120	
acc ggc tgg ggt cgc ctc agt ggc gtg ggc aat gtg aca cca gca cat				529
Thr Gly Trp Gly Arg Leu Ser Gly Val Gly Asn Val Thr Pro Ala His	125	130	135	140
ctg cag cag gtg gct ttg ccc ctg gtc act gtg aat cag tgc cgg cag				577
Leu Gln Gln Val Ala Leu Pro Leu Val Thr Val Asn Gln Cys Arg Gln	145	150	155	
tac tgg gac tca agt atc act gac tcc atg atc tgt gca ggt ggc gca				625
Tyr Trp Asp Ser Ser Ile Thr Asp Ser Met Ile Cys Ala Gly Gly Ala	160	165	170	
ggt gcc tcc tcg tgc cag ggt gac tcc gga ggc cct ctt gtc tgc cag				673
Gly Ala Ser Ser Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Cys Gln	175	180	185	
aag gga aac aca tgg gtg ctt att ggt att gtc tcc tgg ggc acc aaa				721
Lys Gly Asn Thr Trp Val Leu Ile Gly Ile Val Ser Trp Gly Thr Lys	190	195	200	
aac tgc aat gtg cgc gca cct gct gtg tat act cga gtt agc aag ttc				769
Asn Cys Asn Val Arg Ala Pro Ala Val Tyr Thr Arg Val Ser Lys Phe	205	210	215	220
agc acc tgg atc aac cag gtc ata gcc tac aac tgagctcacc acaggccctc				822
Ser Thr Trp Ile Asn Gln Val Ile Ala Tyr Asn	225	230		
cccagctcaa cccatttaaa ggacccaggc cctgtcccat catgcattca tgtctgtctt				882
cctggctcag gagaaagaag aggctgttga gggctccgact ccctacttgg acttctggca				942
cagaagggggc tgagtgactc cttgagtagc agtggctctt cctagagtag ccatgccgtg				1002
gccggggccc ccacccctcc tccagggcaa ccccttggtc ctacagcaag aagccagaac				1062
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 -15 -10 -5

Arg Ile Val Asn Gly Glu Asn Ala Val Leu Gly Ser Trp Pro Trp Gln
 -1 1 5 10 15

Val Ser Leu Gln Asp Ser Ser Gly Phe His Phe Cys Gly Gly Ser Leu
 20 25 30

Ile Ser Gln Ser Trp Val Val Thr Ala Ala His Cys Asn Val Ser Pro
 35 40 45

Gly Arg His Phe Val Val Leu Gly Glu Tyr Asp Arg Ser Ser Asn Ala
 50 55 60

Glu Pro Leu Gln Val Leu Ser Val Ser Arg Ala Ile Thr His Pro Ser
 65 70 75

Trp Asn Ser Thr Thr Met Asn Asn Asp Val Thr Leu Leu Lys Leu Ala
 80 85 90 95

Ser Pro Ala Gln Tyr Thr Thr Arg Ile Ser Pro Val Cys Leu Ala Ser
 100 105 110

Ser Asn Glu Ala Leu Thr Glu Gly Leu Thr Cys Val Thr Thr Gly Trp
 115 120 125

Gly Arg Leu Ser Gly Val Gly Asn Val Thr Pro Ala His Leu Gln Gln
 130 135 140

Val Ala Leu Pro Leu Val Thr Val Asn Gln Cys Arg Gln Tyr Trp Asp
 145 150 155

Ser Ser Ile Thr Asp Ser Met Ile Cys Ala Gly Gly Ala Gly Ala Ser
 160 165 170 175

Ser Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Cys Gln Lys Gly Asn
 180 185 190

Thr Trp Val Leu Ile Gly Ile Val Ser Trp Gly Thr Lys Asn Cys Asn
 195 200 205

Val Arg Ala Pro Ala Val Tyr Thr Arg Val Ser Lys Phe Ser Thr Trp
 210 215 220

Ile Asn Gln Val Ile Ala Tyr Asn
 225 230

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 Leu Ser Leu Val Leu Leu Gly Ser Ser Trp Gly Cys Gly Val Pro Ala
 -25 -20 -15

atc acg cct gca ctg agc tac aat cag aga att gtc aac ggg gag aat 149
 Ile Thr Pro Ala Leu Ser Tyr Asn Gln Arg Ile Val Asn Gly Glu Asn
 -10 -5 -1 1 5

gca gtg cca ggc tcc tgg ccc tgg cag gtg tct ctc cag gat aac acc 197
 Ala Val Pro Gly Ser Trp Pro Trp Gln Val Ser Leu Gln Asp Asn Thr
 10 15 20

ggc ttc cac ttc tgc ggt ggt tct ctc atc agt ccg aac tgg gtg gtc 245
 Gly Phe His Phe Cys Gly Gly Ser Leu Ile Ser Pro Asn Trp Val Val
 25 30 35

acg gct gcc cac tgc caa gtc acg cct gga cgc cac ttt gtc gtt ttg 293
 Thr Ala Ala His Cys Gln Val Thr Pro Gly Arg His Phe Val Val Leu
 40 45 50

gga gaa tat gac cga tct tcc aat gct gaa cct gtg cag gtc ctc tcg 341
 Gly Glu Tyr Asp Arg Ser Ser Asn Ala Glu Pro Val Gln Val Leu Ser
 55 60 65 70

atc gca agg gcc atc aca cac cct aac tgg aac gcc aac acc atg aac 389
 Ile Ala Arg Ala Ile Thr His Pro Asn Trp Asn Ala Asn Thr Met Asn
 75 80 85

aat gac ctg act ctc ctg aag ctt gcc tcg cca gcc cgg tac aca gca 437
 Asn Asp Leu Thr Leu Leu Lys Leu Ala Ser Pro Ala Arg Tyr Thr Ala
 90 95 100

caa gtc tca cca gtc tgc ctg gct tcc aca aac gag gca ctg cct tcg 485
 Gln Val Ser Pro Val Cys Leu Ala Ser Thr Asn Glu Ala Leu Pro Ser
 105 110 115

ggg ctc acc tgt gtc acc act ggc tgg ggc cga atc agt ggt gtg ggc 533
 Gly Leu Thr Cys Val Thr Thr Gly Trp Gly Arg Ile Ser Gly Val Gly
 120 125 130
 aat gtg aca cca gct cgc ctg cag caa gtt gtt cta ccc ctg gtc act 581
 Asn Val Thr Pro Ala Arg Leu Gln Gln Val Val Leu Pro Leu Val Thr
 135 140 145 150
 gtg aat cag tgt cgg cag tac tgg ggt gca cgc att acc gat gcc atg 629
 Val Asn Gln Cys Arg Gln Tyr Trp Gly Ala Arg Ile Thr Asp Ala Met
 155 160 165
 ata tgt gca ggt ggc tca ggc gcc tcc tca tgt cag ggt gac tca gga 677
 Ile Cys Ala Gly Gly Ser Gly Ala Ser Ser Cys Gln Gly Asp Ser Gly
 170 175 180
 ggc cct ctt gtc tgc cag aag gga aac acc tgg gtg ctt att ggg att 725
 Gly Pro Leu Val Cys Gln Lys Gly Asn Thr Trp Val Leu Ile Gly Ile
 185 190 195
 gtc tcc tgg ggc act aag aac tgc aac ata caa gca ccg gcc atg tac 773
 Val Ser Trp Gly Thr Lys Asn Cys Asn Ile Gln Ala Pro Ala Met Tyr
 200 205 210
 act cgg gtc agc aag ttc agt acc tgg atc aac caa gtc atg gcc tac 821
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 Asn

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Trp Gly Cys Gly Val Pro Ala Ile Thr Pro Ala Leu Ser Tyr Asn Gln
-15 -10 -5

Arg Ile Val Asn Gly Glu Asn Ala Val Pro Gly Ser Trp Pro Trp Gln
-1 1 5 10' 15

Val Ser Leu Gln Asp Asn Thr Gly Phe His Phe Cys Gly Gly Ser Leu
20 25 30

Ile Ser Pro Asn Trp Val Val Thr Ala Ala His Cys Gln Val Thr Pro
35 40 45

Gly Arg His Phe Val Val Leu Gly Glu Tyr Asp Arg Ser Ser Asn Ala
50 55 60

Glu Pro Val Gln Val Leu Ser Ile Ala Arg Ala Ile Thr His Pro Asn
65 70 75

Trp Asn Ala Asn Thr Met Asn Asn Asp Leu Thr Leu Leu Lys Leu Ala
80 85 90 95

Ser Pro Ala Arg Tyr Thr Ala Gln Val Ser Pro Val Cys Leu Ala Ser
100 105 110

Thr Asn Glu Ala Leu Pro Ser Gly Leu Thr Cys Val Thr Thr Gly Trp
115 120 125

Gly Arg Ile Ser Gly Val Gly Asn Val Thr Pro Ala Arg Leu Gln Gln
130 135 140

Val Val Leu Pro Leu Val Thr Val Asn Gln Cys Arg Gln Tyr Trp Gly
145 150 155

Ala Arg Ile Thr Asp Ala Met Ile Cys Ala Gly Gly Ser Gly Ala Ser
160 165 170 175

Ser Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Cys Gln Lys Gly Asn
180 185 190

Thr Trp Val Leu Ile Gly Ile Val Ser Trp Gly Thr Lys Asn Cys Asn
195 200 205

Ile Gln Ala Pro Ala Met Tyr Thr Arg Val Ser Lys Phe Ser Thr Trp
210 215 220

Ile Asn Gln Val Met Ala Tyr Asn
225 230

<210> 5
<211> 99
<212> DNA
<213> Artificial Sequence

<220>
<223> Designed oligonucleotide to construct plasmid pSecTrypHis.

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aagcttggct agcaacacca tgaatctact cctgatcctt acctttgttg ctgctgctgt 60
tgctgcccc tttgacgacg atgacaagga tccgaattc 99

<210> 6
<211> 99
<212> DNA

<213> Artificial Sequence

<220>

<223> Designed oligonucleotide to construct plasmid pSecTrypHis.

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gaattcggat ccttgatcatc gtcgtcaaag ggggcagcaa cagcagcagc aacaaaggta 60

aggatcagga gtagattcat ggtgttgcta gccaaagctt 99

<210> 7

<211> 15

<212> DNA

<213> Artificial Sequence

<220>

<223> Designed oligonucleotide primer to amplify neurosin-encoding sequence.

<400> 7

ttggtgcatg gcgga 15

<210> 8

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Designed oligonucleotide primer to amplify neurosin-encoding sequence.

<400> 8

tcctcgagac ttggcctgaa tggtttt 27

<210> 9

<211> 35

<212> DNA

<213> Artificial Sequence

<220>

<223> Designed oligonucleotide primer to amplify a portion of plasmid p SecTrypHis/Neurosin.

<400> 9

gcgctagcag atctccatga atctactcct gatcc 35

<210> 10

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> Designed oligonucleotide primer to amplify a portion of plasmid p SecTrypHis/Neurosin.

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tgaagcttgc catggaccaa cttgcatc 29

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<210> 11
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Designed oligonucleotide primer to amplify a portion of plasmid p
TrypHis.

<400> 11
ccaagcttca ccatcaccat caccat 26

<210> 12
<211> 17
<212> DNA
<213> Artificial Sequence

<220>
<223> Designed oligonucleotide primer to amplify a portion of plasmid p
TrypSigTag.

<400> 12
gcacagtcga ggctgat 17

<210> 13
<211> 17
<212> DNA
<213> Artificial Sequence

<220>
<223> Designed oligonucleotide primer to amplify a portion of plasmid p
FBTrypSigTag.

<400> 13
caaatgtggg atggctg 17

<210> 14
<211> 20
<212> DNA
<213> Artificial Sequence

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<223> Designed oligonucleotide primer to amplify conserved region of se
rin proteases-encoding sequence.

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<221> misc_feature
<222> (9)..(9)
<223> n is a, c, g or t.

<220>
<221> misc_feature
<222> (12)..(12)
<223> n is a, c, g or t.

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gtgctcacng cngcbcaytg 20

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<210> 15
 <211> 20
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Designed oligonucleotide primer to amplify conserved region of se
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 <223> n is a, c, g or t.

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 ccvctrwsdc cncnnggcga 20

 <210> 16
 <211> 20
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Designed oligonucleotide primer for RACE for hBSSP5 (forward).

 <400> 16
 tgtcagccct ggccgccatt 20

 <210> 17
 <211> 20
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Designed oligonucleotide primer for RACE for hBSSP5 (forward).

 <400> 17
 gcgagtatga ccgatcatca 20

 <210> 18
 <211> 20
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Designed oligonucleotide primer for RACE for hBSSP5 (reverse).

 <400> 18
 cgccacctgc acagatcatg 20

 <210> 19

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<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Designed oligonucleotide primer for RACE for hBSSP5 (reverse).

<400> 19
gaatcagtgc cggcagtact                                20

<210> 20
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Designed oligonucleotide primer designated as hBSSP5F1 to amplify
      full length hBSSP5 (forward).

<400> 20
tgccacgatg ttgctgctca                                20

<210> 21
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Designed oligonucleotide primer designated as hBSSP5F2 to amplify
      mature hBSSP5-encoding region (forward).

<400> 21
attgtcaacg gggagaatgc                                20

<210> 22
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Designed oligonucleotide primer designated as hBSSP5R1/E to ampli
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<400> 22
ggaattcggg tctttaatgg gttgagc                        27

<210> 23
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Designed oligonucleotide primer designated as hBSSP5R4 for RT-PCR
      (reverse).

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cctggcacga ggaggcac                                18

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<210> 24
 <211> 20
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Designed oligonucleotide primer designated as mBSSP5F1 for RACE f
 or mBSSP5 (forward).

 <400> 24
 accatgaaca atgacctgac 20

 <210> 25
 <211> 17
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Designed oligonucleotide primer designated as mBSSP5F2 for RACE f
 or mBSSP5 (forward)

 <400> 25
 gaatcagtggt cggcagt 17

 <210> 26
 <211> 20
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Designed oligonucleotide primer designated as mBSSP5F3 to amplify
 full length mBSSP5 (forward).

 <400> 26
 gaccatctca acaccattcc 20

 <210> 27
 <211> 20
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Designed oligonucleotide primer designated as mBSSP5F mature to a
 mplify mature mBSSP5-encoding region (forward).

 <400> 27
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 <210> 28
 <211> 20
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Designed oligonucleotide primer designated as mBSSP5R2 for RACE f
 or mBSSP5 (reverse).

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<210> 29
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Designed oligonucleotide primer designated as mBSSP5R3/E to ampli
fy full length mBSSP5 (reverse).

<400> 29
caggtgtttc ctttctggca 20

<210> 30
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<212> DNA
<213> Artificial Sequence

<220>
<223> Designed oligonucleotide primer designated as mBSSP5R3/E to ampli
dy full length mBSSP5 (reverse).

<400> 30
ggaattcgga cagtttagtt gtaggcc 27

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<211> 117
<212> DNA
<213> Artificial Sequence

<220>
<223> Designed oligonucleotide to construct plasmid pTrypHis.

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tgctgcccc tttcaccatc accatcacca tgacgacgat gacaaggatc cgaattc 117

<210> 32
<211> 117
<212> DNA
<213> Artificial Sequence

<220>
<223> Designed oligonucleotide to construct plasmid pTrypHis.

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gaattcggat cttgtcatc gtcgtcatgg tgatggtgat ggtgaaaggg ggcagcaaca 60
gcagcagcaa caaaggtaag gatcaggagt agattcatgg tgttgctagc caagctt 117

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